

CL2036 US NA SEQ
SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Co., Inc.
Van Dyk, Tina K

<120> Regulator/Promoter for Tunable Gene Expression and Metabolite Sensing

<130> CL2036 US NA

<150> 60/440,965

<151> 2003-01-17

<160> 9

<170> PatentIn version 3.2

<210> 1

<211> 930

<212> DNA

<213> Escherichia coli

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<221> CDS

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ggc tct ttt acc gcc gcc gcc aga cag cta cag atg agc gtt tcg tcc	96
Gly Ser Phe Thr Ala Ala Ala Arg Gln Leu Gln Met Ser Val Ser Ser	
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atc agt cag acg gta tca aaa ctg gaa gat gag ttg cag gta aag ctg	144
Ile Ser Gln Thr Val Ser Lys Leu Glu Asp Glu Leu Gln Val Lys Leu	
35 40 45	
tta aac cgt agc aca cgc agc att ggc ctg acc gaa gcc ggt aga att	192
Leu Asn Arg Ser Thr Arg Ser Ile Gly Leu Thr Glu Ala Gly Arg Ile	
50 55 60	
tac tac cag ggc tgc cgt cgt atg ctt cat gaa gtg cag gat gtt cat	240
Tyr Tyr Gln Gly Cys Arg Arg Met Leu His Glu Val Gln Asp Val His	
65 70 75 80	
gag caa ctg tat gcc ttc aat aac acc ccc atc ggg acg cta cgc att	288
Glu Gln Leu Tyr Ala Phe Asn Asn Thr Pro Ile Gly Thr Leu Arg Ile	
85 90 95	
ggc tgt tct tca act atg gca caa aat gtt ctc gcc ggg ctg aca gcc	336
Gly Cys Ser Ser Thr Met Ala Gln Asn Val Leu Ala Gly Leu Thr Ala	
100 105 110	
aaa atg ctg aaa gaa tac cca ggt ttg agc gtc aat ctg gtt acc gga	384
Lys Met Leu Lys Glu Tyr Pro Gly Leu Ser Val Asn Leu Val Thr Gly	
115 120 125	
att cca gcc ccc gac ctg att gcc gac ggt ctg gat gtg gtg atc cgc	432
Ile Pro Ala Pro Asp Leu Ile Ala Asp Gly Leu Asp Val Val Ile Arg	
130 135 140	
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Val Gly Ala Leu Gln Asp Ser Ser Leu Phe Ser Arg Arg Leu Gly Ala	
145 150 155 160	

CL2036 US NA SEQ

atg cca atg gtg gtg tgc gcc gcg aaa agc tat ctc aca caa tac ggc	528
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ata ccg gaa aaa ccc gcc gat ttg agt agt cat tca tgg ctt gaa tac	576
Ile Pro Glu Lys Pro Ala Asp Leu Ser Ser His Ser Trp Leu Glu Tyr	
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agc gtg cgg ccc gac aat gaa ttt gaa ctg atc gca ccg gaa ggg atc	624
Ser Val Arg Pro Asp Asn Glu Phe Glu Leu Ile Ala Pro Glu Gly Ile	
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tcg act cgc ctg atc cca caa gga aga ttt gtg act aat gat ccg atg	672
Ser Thr Arg Leu Ile Pro Gln Gly Arg Phe Val Thr Asn Asp Pro Met	
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acg ctg gtg cgc tgg ctg acg gcg ggt gcc ggg atc gcc tac gtg ccg	720
Thr Leu Val Arg Trp Leu Thr Ala Gly Ala Gly Ile Ala Tyr Val Pro	
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ctg atg tgg gtg atc aac gag atc aat cgt ggg gag ctg gag atc ctg	768
Leu Met Trp Val Ile Asn Glu Ile Asn Arg Gly Glu Leu Glu Ile Leu	
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ctg ccg cgt tac cag tca gat cca cgc ccg gtt tat gcg tta tat acc	816
Leu Pro Arg Tyr Gln Ser Asp Pro Arg Pro Val Tyr Ala Leu Tyr Thr	
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gaa aaa gat aag ctg ccg ctg aag gta cag gtc gtg atc aac tcg ctg	864
Glu Lys Asp Lys Leu Pro Leu Lys Val Gln Val Val Ile Asn Ser Leu	
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acg gat tat ttt gtt gag gtc ggt aaa ttg ttt cag gag atg cac ggg	912
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Ile Ser Gln Thr Val Ser Lys Leu Glu Asp Glu Leu Gln Val Lys Leu
35 40 45
Leu Asn Arg Ser Thr Arg Ser Ile Gly Leu Thr Glu Ala Gly Arg Ile
50 55 60
Tyr Tyr Gln Gly Cys Arg Arg Met Leu His Glu Val Gln Asp Val His
65 70 75 80

CL2036 US NA SEQ

Glu Gln Leu Tyr Ala Phe Asn Asn Thr Pro Ile Gly Thr Leu Arg Ile
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Gly Cys Ser Ser Thr Met Ala Gln Asn Val Leu Ala Gly Leu Thr Ala
100 105 110

Lys Met Leu Lys Glu Tyr Pro Gly Leu Ser Val Asn Leu Val Thr Gly
115 120 125

Ile Pro Ala Pro Asp Leu Ile Ala Asp Gly Leu Asp Val Val Ile Arg
130 135 140

Val Gly Ala Leu Gln Asp Ser Ser Leu Phe Ser Arg Arg Leu Gly Ala
145 150 155 160

Met Pro Met Val Val Cys Ala Ala Lys Ser Tyr Leu Thr Gln Tyr Gly
165 170 175

Ile Pro Glu Lys Pro Ala Asp Leu Ser Ser His Ser Trp Leu Glu Tyr
180 185 190

Ser Val Arg Pro Asp Asn Glu Phe Glu Leu Ile Ala Pro Glu Gly Ile
195 200 205

Ser Thr Arg Leu Ile Pro Gln Gly Arg Phe Val Thr Asn Asp Pro Met
210 215 220

Thr Leu Val Arg Trp Leu Thr Ala Gly Ala Gly Ile Ala Tyr Val Pro
225 230 235 240

Leu Met Trp Val Ile Asn Glu Ile Asn Arg Gly Glu Leu Glu Ile Leu
245 250 255

Leu Pro Arg Tyr Gln Ser Asp Pro Arg Pro Val Tyr Ala Leu Tyr Thr
260 265 270

Glu Lys Asp Lys Leu Pro Leu Lys Val Gln Val Val Ile Asn Ser Leu
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CL2036 US NA SEQ

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ccagccagaa aatcgccagt gataaaagca attcaaaaaa tatcgggtggg aaggacagcc 180
caaacaccac gataacggga aacagactca tggtgacctt gggtgtaaag agagagcagg 240
cggtattatt ttcagcatct gtcgccgcag agaagggcat ggaaagccgg gcgagagcaa 300
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gtgatctaaa tcacttttaa gtcagagtga ata 393

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CL2036 US NA SEQ

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